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A diverse family of inositol 5-phosphatases playing a role in growth and development in Dictyostelium discoideum

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Appendix A: Amino acids sequences of Dd5P1, Dd5P2, Dd5P3 and Dd5P4.

Amino acids represented in figure 2 are underlined and shown in blue.

Dd5P1

MVLRGRAGSMTPQVNFNKLSGSGNIEERNNNQSSSSQSQSSPSPSQSPSLQQNQLNSSNGM
NNKVKNLLDLENYYKSIKKNITENQFEFSIKKKKEKNRTLLVNLKDKSLTIFKLSKRGKKNK
NIKKYLISEIEKITKDKKDNKELIVFRRSKKKEMKLYFLNTERRECFYELIWMTWNNKIM
PPTPLSGEEDVEEKAQYEKISIFISTWNMGDAPPPINEGLLNSWIPKSKPYDLYVIGVQE
CEYTPLKSKHKQTQLNQFPQQPQFPQFPQQAQAAQQPQQQNQSQQQYSECQEDWFGTLSEHL
GHDYYKVESTSLVKMRILIFAKKQHYKINYIEKASIGTGIGNMYGNKGGTCISLSWWET
SFCFMSHFAAHQEKIEQRNSNYKDIKGIKIGNKELDILNQYNYVFWMGDLNRYIGGGL
FREEVLMHIKSKNIRKLLQHDQLNQORNQEKVFIGFKEEPVGFLEPTYKTLRGVENQYTEE
KQRIPSWCDRIHHKKLPYSHDIICLEYNSANRITTSDHVPVYGVYESYVRMPCSPNSSSSC
SNVKKQICQILFNDLRAECLDMVDNEERAPDAYIVFNSSAFIATEITTPHAYKNRNPIWG
DLPPITPIIERQNFLFTQHLFLTFYHDDKSIGHAAVPLGIGFQKEPFAFKTRITRNLPA
GTLFGSIHIVYNKFLIQN

Dd5P2

MGKRKTGNTCHNIDKKYSPSPSVLISLNLQQLSMGPNHSAAIVNNECLMWGEVMGRKHTT
LFIKIVWKRRVSVSCGFNHTLLLTSEYKIFSMGFNQTGQLGIENVVDSAVPLPVDTLTKF
NVIKIKAGNNVSAAITEAGDLYCWGSSAYGQLGNGKMNAKLHSFTPTTILNPLIPDAEKD
DPIYQNLQYTNICFGAQHTIAISTTGAFISWGSNQYQQLGLGHCNAKLVPVPIHLDNSFE
RRAGHINSLSGEIVTTDFTAKTIHRIVVDIACGNFHSALLTLEGDLFLWGSNQYQGQLGQGD
SLDQSVPKTVKGSLEFVKINRMALGNHTILLTKEQDVFTFGSNEFYQLGHGSIIGKNRL
YFPTQIQPKVMASDIFAAGDCSAYFVLDDSPVHLNLLGQHQLLNGAGNGGGGSSNNN
NNLLNNYNNGLMGSTNKHLSIFVGTWNCNAKRTQNLANWILTNSFAPDIIVLGLQEI
KAGAIKATAADKQNNKENAYHPWKHDIEQTLSSLSSGGRYVKVMNKVLVGLMILVYVKEE
HAPYISEVSGAVVPCGMMGKIGNKGGLGVRFTLYKTGICFVNSHLAAGPSHEKMERRTQD
YKKIQMMTFENHLSMLDHECLIWFGDLNRYIDLPLYSETKALIEQKNWQKLQAHDQLNNER
KAGKAFIGFKEELTNFAPSYKYDIGVNQYDTSEKNRTPSWCDRIIRGESLKQISYQRHE
LME^{SDH}RPI^{SA}IFLLETKEYIHAESSKAWSKFHKHDHANRSDSPDPFFSKIGSAAHHFSP
VELKSSSSSINSTNSSVDSLVSISSSNTTNTSTNTTDSINIINTSTKRNLPLNPAPPLP
PKSNAVKKSLLLNIHQHSHSGSGSIGGSSSGNPFVVGSMPTFSPHFMYSNSPTSSDTSTN
SGVTLNDSPMIRSILKNNAINKRLSFAEDIHSVKVLSNHRKIKLN?NNNNNNNNNNNNNN
N?NNNNNNNNNNNNNNNNNNNGDNKNNNEVGNINNNNNNEV?NINNINNNNNNNNNNSNDI
NNNSNLIIEKEINNKSQQQQEEETNSPNLQPTDNSNSTNTRPPSSSLLSSVINSLETATS
IDSPPMFSLNSDDNVDSSMENRNFNDNEYIGQNNVNNEKDNHNSHHNVDDVDDDDVIIII
KPMQOKTIVDRKGKRKTIVLINTFDSIDSLGGSEALEIAKDSLNYPHHTDDEEDEDGDDDE
EEEEEEDEEDEDDEFIDSESDSDVGGYCSSMPTLNSLGDGACHLEDLPLNFLKNREINYG
YDHIGHSSSSNNSTNNLGDYISSISPRAITSTTLTKNPKQEI^{ER}ELENSVNNSNNNSI
NNNSNNNNNNNTNNNNNTNNNNNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNSDKNSDSEASIGSGILGNIDDIQNIIGNIKNGDQVNKNLNHKKSNSVEVVV
VEHHDEENCSDNIFYIEPFTIVDQYTNNNNNNNNNNNNNNNNNNNNNNNNNNNDNNNDNNNDND
NNDNNNSGATITITPRSSPIKDELKSMIRNSLSGLEPMVVSSSNTPPIVSSPSVNTITP
KQSPSS?S?QSLKNESEFICVSPSSPSRVLFNPIFDKSFFEQKHRVVNTDIVLGSH?RSS
PPVISPIGEFNSTTNTSTNTSTT?STTNSNSNINTKTNAINNKNKSDRELDKLKTSGGSS
FINIKSANSSRNNSMIYHSIENRHNNYNSDDSEDDGISYNINSDSDSDSDSHSDTNENSN
INIEPKTIEPKIIIEPTTSIATTTEPTTSTEIETNTTVTTSTDPKLPTKEGSSSL

Dd5P3

MADNTFRIFITTSQSFIIKRDSLHASKALVINRRDPSKIDIIQPDQIDQSLRSERSVYCVLG
IFRLVNECYLVVVTESDIAANFQFQGGQPNVIRKIRCTDFISFQTGRGHISIGGGGGGGGS
GNGESKEDDRPYVQVMNLLNSGHFYWTPPNSSFDITRTYQSQCLEPKSDLPVWERVDKRF
YWNKYLQKDFIAYRLYDWCFFPIIQGFVVSDHLGHIQGNVVTILISRRSRFRAGTRFVTR
GIDDDGNVANFCESEQILSIESYGVLAFLQIRGSVPVFWNQSSPQMSDLKIKMSNLKIG
KISKKKITTIARNTQATTPAFQLHLKEQTKKYGNIVIVNLLSKLKSCECDLVNAYEEQIRI
LRSPQVFYNHFDLNEQTKGNRMDPLDSLINYIDNQSISGGGGTTGGVSEKIVGYFFQNSN
GQIISKQNGIIRTNCKDCLDRTNIVQSRVSWVLFESQLRKLGLFRGHDSIGSYPRVSQTL
KTTWADNGDALSIQYAGSGSLKSTLTREGDYGIMGMLADGKKTMTRFYINNFEDEPGRQDV
LDLLLGLHKSMMVNNSNNGNGGNGSGHDDNIRKQVQDRVKEYSKKEWRNVFVGTYNV
GGVHSSYFDLVQWLRPDGANCPTPDEFYVLGLQEVVELTAGQILATDSSIGKWEDAIERA
LPKVSPNVKYIKLQSSQLVGLLMAIYVREDAIHYFREVQIQNVKCGMNLGAGNKGIGVR
LLFSDTSFTFVTAHFAAGQSNVEDRISDFREIDSTLAFGRQGQFKVSDSDYSFWLGDFNF
RIDLPDEEIRRCVYDQQFPKLYNYDQLRKCMERGVFNQYREETIAFPPTYKYDLNSTQY
DTSQKQRSPAWTDRIVWSNKVHHDLRQLYYHRQEILASDHRPVSSYFQLEVTKIDKDKER
TLRQELYEQKSSQFITTSQSTNNLINTTNQNGKDGANLITKEFEQLTLIKQSASTPNLQK
GRSNTTNIQYQITSTNQISNTNNNTIQQQQHHQELVNVTTTRKNSLNSNNNNNNNNINNS
NNTLVASGGSGNGVPPRKLSSGRPLPMLPQPIQIPPTQQQQQQQQQQQQQQQQQETVNLQKM
TGSGGGRKISSPSSSFNNTNSIGSSSSPSGAHSPIFDDQFDPKGRSSPVPQSFNENNN
SNQSKMELLIPNQNSTQYQQQQQQQQQQQQQQQQQQQQQQQQQQPQYNSNLNSGPPP
LQPIHQSNLNPNSNYNQQLQQPPPPQPINHDLQLIDSWGNSNGYQSREPPPLQPIPQSVY
QSQPPPLQPIPQSVYQPTNFALQQPLQPMMSPPPLLYSNQKAVYNIPVPSPYNQQQQQPQ
QPYQQPYQQPYQQPYQQNLYNQPPPLNNSYNNYNNQNNNNNNNNNNNTYNNPYLGSILD

Dd5P4

MGDIQNTDNIESNIDNNNNNNVSLESSSSSQNNNTNTTTTTTTTTTSVDNLQVGVLSISDQS
TPTIETPNQQQQQQQDDNNRGVSNETIKASLDGLKHNSLKTTFPNSTNHQYIDVNTQWIT
NKLKERESEFTEKRGMSIFLGTWNVNGKKPSES LDPWLKDPSMSLQFDIYAIGFQELDLT
AEALLLGDTTRSLPWEQHILNTLQGDYVKLLSKQLVGILLCVYVKKEHKPHIANVQSDIA
AVGIMGMMGNKGGVAIRFSFYNTTICILNSHLNAHMDNVLRNQDMKDISKNIKFINESS
TDHSTINIFDHDQLFWIGDLNYRIPLPDNEVKEKIKKKDFYNLFVLDQLNQMKAGAVFE
GFQEPPIISFAPTYKYDAGTEEYDSSEKKRTPAWCDRILWKTHKAENVGILSYKRAELIS
SDHRPVSAFVVIKIVVIPDSKNRIYQEI VKELDKKENDSMPDANISTNMVDFETIKFMQ
PISKQLIFENIGQVIARFQFIPKLD ETILCKPWLKISPLAGMMIPKEKVTIDLTIIYVDNL
TSGLFNINNNSTNSTNESMDDILILHLENGKDYFISISGKFQKTCFGNTLDNLVRYPHPI
RNNLPIPEQKKLSIPKELWRIIDYIYYNGLKEEGLFIKSGVTKEMELIRDCLDTAEPFS
SISFSIHSMAETLIRFLES LVEPVIPFNMYQQALDASSSPLSCKTLVSHLPSVNYNVFFY
LISFLIETLSNQKENDLKPQDLAIIFSTVLLRPS PQS QLSQFPPDATTVKKKADLILHFL
ISKDLIN

Appendix B: **Amino acids sequence alignment of the catalytic domains of inositol 5-phosphatases.** First two letters indicate the species: At, *Arabidopsis thaliana*; Ce, *Caenorhabditis elegans*; Dd, *Dictyostelium discoideum*; Dm, *Drosophila melanogaster*; Ec, *Encephalitozoon cuniculi*; Hs, *Homo sapiens*; Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*. Genebank entries: AtQ9SKB7, Q9SKB7; CeUnc26, Q9GT42; CeCAB02743 (Synaptojanin-like), CAB02743; Dd5P1, pending; Dd5P2, pending; Dd5P3, pending; Dd5P4, pending; DmO46094 (OCRL-like), O46094; DmQ9W296 (Synaptojanin-like), Q9W296; EcCAD25856, CAD25856; HsTypeI, Q14642; HsSHIP2, O15357; HsOCRL, AAA59964; HsINPP5b, P32019; ScINP52p, NP_014293; SpSyj, I19Y_A. Conserved regions are shown in black (100% conserved), gray with white letters (80-100% conserved) or gray with black letters (60-80% conserved).

	1	*	20	*	40	*	60
Dd5P1	ISIFISTWNMGDAPP-----PINEGLINSWIPKSKPY-----						DLYVIG
Dd5P2	LSIFVGTWNCNAKRT-----QNLANWILTNSFAP-----						DIIVLG
Dd5P3	RNVFVGTYNVGGVHS-----SYFDLVQWLRPDGANCPTP-----						DFYVVG
Dd5P4	MSIFLGTWNVNGKGP-----SESLDPWLKDPMSMLQP-----						DIYAIG
HsTypeI	TAVLLVTANVGSFLD-----DPENLQKNWIREFYQVVHCHKP-----						HFMAIH
HsSHIP2	ISVFIGTWNMGSVPP-----PKNVTSWFTSKGLGKTLDEVTVTIPH-----						DIYVFG
HsOCRL	FRFFVGTWNVNGQSP-----DSGLEPWLNCDPNPP-----						DIYCIG
HsIPP5b	FRFFAGTYNVNGQSP-----KECLRLWLSNGIQAP-----						DVYCVG
DmQ9W296	ARVAVGTYNVNGGKH--FRSIVFKDSLADWLLDCHALARSKALVDVNNPSENVDPV						DIYAIG
CeUnc26	IKIFVGTWNVNGGKNIHNVAFRNESSLSHWIFANSMTRLVSVEDEQLA-----						DIVAIG
ScINP52p	INLFVGTWNVNGNSR-----RADLSKWLFPIDGKFKP-----						DVVVLG
SpSyj	VKIFVASYNLNGCSA-----TTKLENWLFPEPTPLA-----						DIYVVG
DmO46094	IIIIYCATWNVNNTCTC-----SDSNPLRAWLACSEKPP-----						DIYAIG
CeCAB02743	VKICVSTFNVNGRSP-----LSVFPTWFSQKPEDIA-----						EFYAVG
AtQ9SKB7	VKILIGTWNVGEGRA-----SRGALVSWLGSVAVSDV-----						GIVAIG
EcCAD25856	MLVTVLSSWNVNNREG-----VADTIS-----						RILGHG
	*	80	*	100	*	120	
Dd5P1	VQCEYTPLSKXHKQTQLNQPPQQPQPQPQQAQAQQQPQQQNQSQQQYSECQED					WFGTILSEHL	
Dd5P2	LQEI-----VNMKAGAIVKATAADKQNNKENAYHPWKHDI EQTL						
Dd5P3	LQEV-----VELTAGQILATDSSIGKQWEDAIERAL						
Dd5P4	FQEL-----DLTAEALLLGDITRSLPWEQHILNTL						
HsTypeI	CQEF-----GGKNEYEASMSHVDFVKELLSSDAMKEYNRARVYL						
HsSHIP2	TQEN-----SVG-----DREWLDLIRGGL						
HsOCRL	FQEL-----DLSTEAFFYFESVKEQEWMAVERGL						
HsIPP5b	FQEL-----DLSKEAFFFHDTPKKEEWFKA VSEGL						
DmQ9W296	FEEI-----VDLNASNIMAASTDNAKLWAEELQKTI						
CeUnc26	VEEL-----VDLNASNVMKASTTNQRMWCESIRKTL						
ScINP52p	LQEV-----IELTAGSILNADYTKSSFWEETMVTDCI						
SpSyj	FQEI-----VQLTPQQVISADPAKRREWESCVKRLI						
DmO46094	LQEL-----DTPTKAMLNSTQVQAIEKQWIDKMMDSV						
CeCAB02743	LQEM-----DLSVGTYIIDNTKKMEGWVDAIHCSL						
AtQ9SKB7	LQEV-----DMGAGFLAMSTAKETVGVEGSAVGQWLLDAIGNAL						
EcCAD25856	ESDM-----ILISLQEHFDFYSGVVRSVLKMV						
	*	140	*	160	*	180	
Dd5P1	-----GHDYYKVESTSLVKMRII-IFAKKQHYYKINYI--EKASIGTGIG-----						
Dd5P2	S--LSSGGRYVKVMNKVLVGLMIL-VYVKEEHAPYI SEVSG--AVVPCGMM-----						
Dd5P3	P-KVSPNVKYIKLQSSQLVGLLMA-IYVREDAIHYFREVQI--QNVKCGMN-----						
Dd5P4	Q-----GDYVKLLSKQLVGILLC-VYVKKKEHKPHIANVQS--DIAAVGIM-----						
HsTypeI	DENYKSQEHTALGSFYFLHESLKNIIYQFDFKAKKYRKVAG-KEIYSDTLESTPMLEKEKFPQ						
HsSHIP2	KELTD--LDYRPIAMQSLWNKIVA-VLVKPEHENRISHVST--SSVKTGIA-----						
HsOCRL	H----SKAKYKKVQLVRLVGMMLL-IFARKDQCRYIRDIAT--ETVGTGIM-----						
HsIPP5b	H----PDAKYAKVKLIRLVGIMLL-LYVKQEHAAAYISEVEA--ETVGTGIM-----						
DmQ9W296	S---RDNDYVLLTYQQLVGVCCLY-IYIRPEHAPHIRDVAI--DCVKTGLG-----						
CeUnc26	S---EKAPFVLIGSEQLVGVCCLF-LFARPRVSPYLKDFAV--ASVKTGMG-----						
ScINP52p	N---QYEEKYLLLRVEQMSSLLIL-FFARSDRAYNIKEVGG--STKKTGFG-----						

SpSyj	NGKCTSGPGYVQLRSGQLVGTALM-IFCKESCLPSIKNVEG--TVKKTGLG-----
Dm046094	H----PDVEYEILMSHRLVATMLT-VIVRKQLRQHIIIRCP--KSARGIF-----
CeCAB02743	P---GGRTQFNVVGSMRLVGIFVI-VFQAVNSKVRVSDVNV--KYVATGISVL-----
AtQ9SKB7	D---ERNTFERMGSRLAGLLIS-LWVRKSIRTHVGDLDV--AAVPCGFG-----
EcCAD25856	P-----SYKMVSADRVLGLWSI-VLSKERHSTTVMKIGL--GFL--G-----

	*	200	*	220	*	240	*
Dd5P1	-----	NMYGNKGGTCTISLSW	WETSFCFMSSHFAAHQE--	KIDQRNSNYKDI	IKGIKIGN----		
Dd5P2	-----	GKIGNKGGGLGVRFTLYKTGICFVN	SHLAAGPSHEKMERRTQDYKKIQ--	MMTFEN----			
Dd5P3	-----	GLAGNKGGIGVRLLFSDTSFTFVTAHFAAGQS--	NVEDRISDFREIDSTLAFGR----				
Dd5P4	-----	GMMGNKGGVAIRFSFYNTTICILNSHLNAHMD--	NVLRNQDMKDISKNIKFIN----				
HsTypeI	DYFPECKWSRKGFIRTRWCIADCAFDLVNIHLFHDAS---	NLVAWETSPSVYSGIRHKA----					
HsSHIP2	-----	NTLGNKGAVGVSMFMNGTSFGFVNCHLTSGNE--	KTARRNQNYLDILRLLSLGD----				
HsOCRL	-----	GKMGNKGGVAVRFVFHNTTFCIVNSHLAAHVE--	DFERRNQDYKDICARMSFVV----				
HsIPP5b	-----	GRMGNKGGVAIRFQFHNTSICVNVNSHLAAHIE--	EYERNNQDYKDICSRMQFCQ----				
DmQ9W296	-----	GATGNKGACAIRFVLHGTSMCFVCAHFAAGQS--	QVAERNADYAEITRKLAFPM----				
CeUnc26	-----	GATGNKGSVAFRIVVFSTSI	CFICSHFAAGQN--EIRDRNEDFATTLKKIRFPL----				
ScINP52p	-----	GITGNKGAVAIRFDYGATSFCFVNTHLSAGAS--	NIDERRNDYNNIYRNITFPR----				
SpSyj	-----	GVS	GNKGAVAIRFDYEDTGLCFITSHLAAGYT--	NYDERDHDYRTIASGLRFRR----			
Dm046094	-----	NTLGNKGGVAISLQLNEGNICFVN	SHLAAHMG--YVEERNQDYNAIVEGIRFDD----				
CeCAB02743	-----	VNKLGNKGGTAVSMKMNDTWCFVNAHFAAGNN--	ELERNNQDFRDIYNDMVFP----				
AtQ9SKB7	-----	RAIGNKGGVGLRIRVYDRIMCFVNCHLAHLE--	AVTRRNADFNHIYRSMVFSKGQSV----				
EcCAD25856	-----	FINKGACVTRISN--GVMFISCHLSAHQE--	NSKKRQEEIRKVFECTICDEE----				

	260	*	280	*	300	*
Dd5P1	-----	KELDI	LNQYNYVFWMGDLNYRIG-----			
Dd5P2	-----	HLSMLDHECL	IWF	GDLNYRID-----		
Dd5P3	-----	QGQFKVSDSDYSFWL	GDFNFRID-----			
Dd5P4	-----	ESSTDHSTINIFDHDQLFWI	GDLNYRIP-----			
HsTypeI	-----	LGYVLDRIIDQRF	EKVSFVFGDFNFRLDSKSVVETLCTKATM			
HsSHIP2	-----	RQLNAFDISLRFTHLFWF	GDLNYRLD-----			
HsOCRL	-----	PNQTLPLQLNIMKHEVVIWL	GDLNYRLC-----			
HsIPP5b	-----	PDP	SLPPLTISNHDVILWL	GDLNYRIE-----		
DmQ9W296	-----	GRTLKSHDWVFWC	GDFNYRID-----			
CeUnc26	-----	GREIDSHDVI	FWLGDFNYRIN-----			
ScINP52p	-----	SKTIPH	HDSLFWLGDLNYRIT-----			
SpSyj	-----	GRSIFNHDYV	VWFGDFNYRIS-----			
Dm046094	-----	GRTISDHDHIFWV	GDLNYRIQ-----			
CeCAB02743	-----	RSQQEGLRDRPLEVPIMCLYDHDV	VWFGDLNYRLN-----			
AtQ9SKB7	YTA	AAGASTSAQALKNNPNNTNNSTEE	EKSHLASADLVAFFGDFNYRLF-----			
EcCAD25856	-----	SLKGIDTVVLAGDMNFRVS-----				

	320	*	340	*	360	*
Dd5P1	---GGLFREEVLMHIKSKN---	IRKLLQHDQLNQORNQEKVFIGF-----				
Dd5P2	----LPYSETKALIEQKN---	WQKLQAH	DQLN	NERKAGKAFIGF-----		
Dd5P3	----LPDEEIRRCVYDQQ---	FPKLYNYDQLRK	CMEAGRVFNGY-----			
Dd5P4	----LPDNEVKEKIKKKD---	FYNLFLVDQLNQ	QMKAGAVFEGF-----			
HsTypeI	QTVRAADTNEVVKLI	FRES---DNDRKVMLQLEKKLFDYFNQEV	FRDNNGTALLEFDKELSVF			
HsSHIP2	----MDIQEILNYSRKE---	FEP	LLRVDQLNLEREKHKVFLRF-----			
HsOCRL	---MPDANEVKS	LINKKD---LQRL	LKFDQLNI	QRTQKKA	FVDF-----	
HsIPP5b	---ELDVEKVKKLI	EEDK---FQML	YAYDQLKIQ	VAAKTVFEGF-----		
DmQ9W296	----MEKDELKECVRNGD---	LSTVLEFDQLRKEQEAGNV	FGEF-----			
CeUnc26	----LSGDEVKNAVRNGD---	YAKLVENDQLTQ	KALGQTFVGF-----			
ScINP52p	----LTNDEVRR	ELRAQKDG	YIDRLQYDQLTQE	INEGVVFQGF-----		
SpSyj	----LTYEEV	VPCIAQ	GK---LSYLFEYDQLNKQMLT	GKVF	PFF-----	
Dm046094	---EPPGQQRPGPLSDAQT---	YEL	LLQYDQLRQEMRRGKCFEGY-----			
CeCAB02743	TD	MYGISNDEVRR	RIASSDK---FADLLQHCQLRE	QMARGTVFKDF-----		
AtQ9SKB7	---GITYDE	ARDFI	SHRS---FDWLREK	DQLRQEMNEGKVFQGM-----		
EcCAD25856	-----	GVPRALD---	YSRARPGDQCNEFR---	RAYPTF-----		

	380	*	400	*	420	*	440	
Dd5P1	---KE-	EPV	GFLPTYKTL---	RGVENQY	TEEKQ-----	RIPSWCDRILHKKLPYSHD---		
Dd5P2	---KE-	ELTNF	APSYKYD---	IGVNQY	DTSEKN-----	RTPSWCDRIIYRGES-----		
Dd5P3	---RE-	ETIAFP	PTYKYD---	LNSTQY	DTSQKQ-----	RSPA	WTDRI	VWSNKVHHD---
Dd5P4	---QE-	PPISF	APTYKYD---	AGTEEY	DSSEKK-----	RTPAWCDRILWKTHKKAEN---		
HsTypeI	KDR	LYE-	LDISF	PPSPYS---	EDARQGEQYMNT-----	RCPAWCDRILMSPSAKELVLR		

HsSHIP2	----	SE	EEISFPPTYRYE	---	RGSRDTYAWHKQKPTGVRTNVPSWCDRILWKSYPETH	----
HsOCRL	----	NE	GEIKFIPTYKYD	---	SKTDRWDSSGKC	-----RVPAWCDRILWRGTN-----
HsIPP5b	----	TE	GELTFQPTYKYD	---	TGSDDWDTSEKC	-----RAPAWCDRILWKGN-----
DmQ9W296	----	LE	GEITFDPTYKYD	---	LFSDDYDTSEKQ	-----RAPAWTDRVLWRRRKALAEGDF
CeUnc26	----	NE	GQLTFAPTYKYD	---	TFSDDYDTSEKC	-----RAPAWTDRILWKDQRKKGK---
ScINP52p	----	KE	PTLQFRPTYKYD	---	YGTDNYDTSEKA	-----RTPSWTDRIIYKGEN-----
SpSyj	----	SE	LPITFPPTYKFD	---	IGTDIYDTSDKH	-----RVPAWTDRIILYRGE-----
DmO46094	----	TE	GEIKFRPTYKYD	---	PGTDNYDSSEKQ	-----RAPAYCDRVLWKGTR-----
CeCAB02743	----	EE	PSTLPFRPTYKYD	---	CGTNTWDTSEKG	-----RVPAWTDRIILTFKKYPQVGLES
AtQ9SKB7	----	RE	ALITFPPTYKFEKNKPGLGGYDSGEKK	-----	RIPAWCDRVIYRDNQSI SYTEC	
EccAD25856	----	LE	EVIRFGPTYKY	-----	ITGTDELCKR	-----RHPSWCDRVFVSSSCT-----

			*		460		*		480																												
Dd5P1	-----	I	I	C	L	E	Y	N	S	-ANRITTSDHVPVYGVYESYVRMPCSPNSS																											
Dd5P2	-----	L	K	Q	I	S	Y	Q	--R	HELMESDHRPISAIFFLETKEYIHAESS																											
Dd5P3	-----	L	R	Q	L	Y	Y	H--R	QEILASDHRPVSSYFQLEVTKIDKDKER																												
Dd5P4	-----	V	G	I	L	S	Y	K--R	AELISSDHRPVSAFVIKIKVVIPDSKN																												
HsTypeI	E-----	S	E	E	K	V	V	T	Y	DHIGPNVCMGDHKPVFLAFRIMPAGAKPHAHV																											
HsSHIP2	-----	I	I	C	N	S	Y	G	C-T	DDIVTSDHSPVFGTFEVGVT SQFISKKG																											
HsOCRL	-----	V	N	Q	L	N	Y	R	S-H	MELKTSDHKPVSA LFHIGVKVVDERRYR																											
HsIPP5b	-----	I	T	Q	L	S	Y	Q	S-H	MALKTSDHKPVSSVFDIGVRVVD ELYR																											
DmQ9W296	AASA---	W	N	P	G	K	L	I	H	Y	G--R	SELKQSDHRPVIAI IDAEIMEIDQRRR																									
CeUnc26	-----	T	Q	L	L	S	Y	D--R	SELKTSDHRPVGAVFKVETFKVGRKCV																												
ScINP52p	-----	L	H	P	L	A	Y	S--D	A	P	L	K	I	S	D	H	K	P	V	Y	A	A	Y	R	N	V	K	F	V	D	E	K	E	K	L		
SpSyj	-----	L	V	P	H	S	Y	Q--S	V	P	L	Y	Y	S	D	H	R	P	I	Y	A	T	Y	E	A	N	I	V	K	V	D	R	E	K	K	K	
DmO46094	-----	I	E	Q	L	A	Y	N	S-I	M	E	I	R	Q	S	D	H	K	P	V	Y	A	V	F	Q	V	K	V	K	T	R	D	E	V	K	Y	K
CeCAB02743	I-----	R	P	M	V	S	I	D	T----	I	T	I	S	D	H	K	P	V	R	A	M	F	N	L	K	V	K	K	I	N	E	S	G	A	N		
AtQ9SKB7	SLKCPVV---	S	S	T	I	M	Y	E	A-C	M	D	V	T	E	S	D	H	K	P	V	R	C	K	L	H	A	N	I	A	H	T	D	K	S	V	R	R
EccAD25856	-----	C	R	F	N	T	Y	S	S-I	H	S	V	K	I	S	D	H	K	P	V	V	C	I	F	E	V	D	G	K	R	T	N	R	I	A	I	P

Appendix C: **Amino acids sequence alignment of RCC1 domains.** First two letters indicate the species: Dd, *Dictyostelium discoideum*; Dm, *Drosophila melanogaster*; Hs, *Homo sapiens*; Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*. Genebank entries: Dd5P2, pending; DmBj1, P25171; HsRCC1, CAA31182; ScPrp20, P21827; SpPim1, P28745. Conserved regions are shown in black (100% conserved), gray with white letters (80-100% conserved) or gray with black letters (60-80% conserved).

	1	*	20	*	40	*	60
HsRCC1	GLVLT	LGQGDV	GLGLG	----	ENVMERKKPALV	SIPED	--VVQAEAGGMHTVCLSKSGQVVSFGCN
DmBj1	GNVLV	CGNGDV	GLGLG	----	EDILERKRLSPV	AGIPD	--AVDISAGGMHNLVLTSGDIYSFGCN
SpPim1	LNVIY	FGSGSM	NELGMG	--	EEEMDVVYRPLN	PILSTD	KVGVVDLAVGGMHSAALLHDGRVYTWGVN
ScPrp20	LDIFC	WGTGSM	CELGLG	PLAKN	KEVKRPRLN	PFLPRDEAKI	ISFAVGGMHTIALDEESNVWSWGCN
Dd5p2	DQLSM	GPNHSA	AIIVNNE	CLMWGE	VMGRKHTT	LFKIVWKRRV	VSVCGFNHTILLTSEYKIFSMGFN
		*	80	*	100	*	120
HsRCC1	DEGAL	GRDTS	VEG	-----	SEMPGKVE	-----	LQE--KVVQVSAGDSHT
DmBj1	DEGAL	GRDTS	EDG	-----	SESKPDLID	-----	LPG--KALCISAGDSHS
SpPim1	DDYAL	GRLTKD	QK	-----	DENGDKVDNDL	--	LEGTPSKVEG---ALSH-LRVTKVICSDNLT
ScPrp20	DVGAL	GRDTS	NAKEQL	KDMDADD	SSDDEDG	DLNELESTPAKIP	RESFPPLAEGHKVVQLAATDNMS
Dd5p2	QTCQL	GIENV	VDS	-----	AVPLPVD	T-----	LSK-FNVIKIKAGNNVS
			*	140	*	160	*
HsRCC1	AALIT	DDGRV	FLWGS	FRDNN	GVIG	---	LLEPM---KKSMPVPVQVQLDVP-----VVKVASGN
DmBj1	ACLLE	DGRV	FAWGS	FRDSH	GNMG	---	LTIDG---NK-RTPIDLMEGTV-----CCSIASGA
SpPim1	AAITD	NGCCFT	WGTFR	CSDG	VLG	---	YSDS---QKRTAEPTQMLRPE-----ICQLATGT
ScPrp20	CALFS	NGEVYA	WGTFR	CNEG	ILG	---	FYQDKIKIQKTPWKVPTFSKYN-----IVQLAPGK
Dd5p2	AAITE	AGDLY	CWGS	--	SAYGQLG	NGKMN	AKLHSFTPTTILNPLIPDAEKDDPIYQNLQYTNICFGA
		*	200	*	220	*	240
HsRCC1	DHIVM	LTA	DGDLY	TLCG	GEQG	QLGRV	PELFANRGGRRQGLERLLVPKCVMLKSRGSRGHVR-----
DmBj1	DHIVIL	ITAGK	VFTVG	CAEQ	QLGRL	SERSIS	GEGRRGKRDLIRPTQLIITRAKP-----
SpPim1	DHIIA	LITTT	GKVYT	WGNG	QQFQ	LGR	-----MLERRRLQGLTPQPPIAKNIIIS-----
ScPrp20	DHILF	LDEEG	MVFA	WNGQ	QNQL	GRK	-----VMERFRLKTLDPFPFGLRHVKY-----
Dd5p2	QHTIA	ISTTG	AIFSW	GSNQ	YGQL	GLGHC	-----NAKLVPVPIHLDNSFERRAGHINSLG
		*	280	*	300	*	320
HsRCC1	-----	FQDA	FCGAY	FTFA	-ISHE	GHVYGF	GLSNYHQLG-----TPGTESC
DmBj1	-----	FEAL	WATNY	CTFM	RESQT	QVIWAT	GLNFKQLAHE---TKGKEFALTPIKT---
SpPim1	-----	VGAG	SYHS	FA-ID	NKGR	VYAWGL	NITROCGIEVEDEEGAVITKPTLV
ScPrp20	-----	IASG	ENHC	FA-L	TKDN	KLVSW	GLNQFGQCGVS-EDVEDGALVTKPKRIALP
Dd5p2	TTDFT	AKTIH	RIVVD	IACG	NFHS	AL-LT	LEGDLFLWGSNQYGQLGQG-----DSL
		*	340	*	360	*	380
HsRCC1	KNSTK	SWVGF	SGGQH	HTVC	MDSEG	KAYSL	GRAEYGRGLGLGEGA-----EE-----KSIPTLIS
DmBj1	--ELK	DIRHI	AGGQH	HTVIL	TTDL	KCSV	GRPEYGRGLGLGDV-----KDV-----VEKPTIVK
SpPim1	--EGY	NVKS	ITGGE	HHTL	LALLED	GRVL	AWGRDDRHLQGLIPDNALPETVVKDEKGNYYLSTPTIIP
ScPrp20	--DNV	VIRSI	AAGEH	SLIL	SQGD	LYSC	GRLDMEVGI
Dd5p2	L-EFV	KINRM	ALGNN	HTILL	TKEQ	DVFTF	GSNEFYQLGHGSIG-----GKNR-----LYFPTQIQ
		*	400	*	420	*	440
HsRCC1	RLPA--	VSSV	ACGAS	VGYAV	TKDGR	VFAW	GMGTNYQLGTGQ-DEDAWSPVEMMGKQLENRVVLSVS
DmBj1	KLTEK	-IVS	VGCGE	VCSY	AVTID	GKLY	SWGSGVNNQLGVGD-GDDELEPIVVVSKNTQGKHMLLAS
SpPim1	GLTN--	VIQV	CGT	HHNL	AVTSD	GKVYS	WGSAAENYEVGQGDNDEDVAVPTLVRSKAIKEVAIRVAG
ScPrp20	NVPK--	FKS	VAAAG	SHSV	AVAQ	NGIAYS	WGFGETYAVGLGPFEDDTEVPTRIKNTATQDHNIIILVG
Dd5p2	KPKVM	ASDIF	AAGDC	SAYF	VLD	DDSPV	HLNLLGQH-QLLN
		*	460	*	480	*	500
HsRCC1	SGGQ	HTV					

DmBj1	GGGQHAI
SpPim1	AGGQFSI
ScPrp20	CGGQFSV
Dd5p2	MGSTNKH

Appendix D: **Amino acids sequence alignment of Sac1 domains.** First two letters indicate the species: Dd, *Dictyostelium discoideum*; Hs, *Homo sapiens*; Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*. Genebank entries: Dd5P3, pending; HsSac1, NP_054735; HshSac2, NP_055752; ScINP52p, NP_014293; SpSyj, I19Y_A. Conserved regions are shown in black (100% conserved), gray with white letters (80-100% conserved) or gray with black letters (60-80% conserved).

	1	*	20	*	40	*	60																																																								
HsSac1	-----MTGP	I	VYV	Q	NADG	I	FFKLAEG	----	KGT	NDAVIHLANQDQGV	---VLG	----	AEE	FP-VQ																																																	
HshSac2	MELFQA	KDHY	ILQ	Q	GERAL	WCSR	RDGGL	QLRPAT	DLLAWN	PICL	GLVEGVIGKIQ	LHSDLP	-WW																																																		
SpSyj	-----MQ	CLLR	-EK	PRSL	ALVN	KDH	ALMFH	SVPQ	NKNSL	SVCVA	EFTA	-----LSE	KPLEG																																																		
ScINP52p	-----MK	IL	SK	Q	TRK	IAI	VSETHGL	VFRP	INSK	NSRR	STCA	VELVP	-----KAEL	NGNG																																																	
Dd5P3	-----MAD	NTRF	RIFIT	TQS	FII	KRD	-S-	LH	SKAL	VINRR	DPSKID	IIQ	-----PD	QID-QS																																																	
		*	80	*	100	*	120	*																																																							
HsSac1	GEV	V	KIAS	L	M	G	F	I	K	----	L	KLN	RYA	II	A	N	T	V	E	E	T	G	----	R	F	N	G	H	V	F	----																																
HmhSac2	LIL	I	RQA	L	V	G	K	L	P	G	D	H	E	V	C	K	V	T	K	I	A	V	L	S	L	S	E	M	E	P	Q	D	L	E	L	E	L	C	K	H	H	F	G	I	N	K	P	E	K	I	I	P	S	P	D	D	S	K	F				
SPsyj	FRK	I	S	S	H	R	I	Y	G	T	L	G	-L	I	E	L	E	G	S	N	F	L	C	V	I	S	G	A	S	E	V	A	R	----	V	R	D	K	E	R	V	F	R	I	M	E	V	C	F	Y	S	V	----	N	R	S	N	W					
ScINP52p	FRR	L	S	N	H	E	I	Y	G	F	I	G	-L	I	E	I	E	G	L	M	F	I	A	T	I	T	G	K	S	K	V	A	Q	----	P	I	P	N	K	T	V	N	K	I	Y	A	V	D	D	F	F	C	L	----	N	N	S	K	W				
Dd5P3Sac	LR	--	S	E	R	S	V	Y	C	V	L	G	-I	F	R	L	V	N	E	C	Y	L	V	V	T	E	S	D	I	A	A	N	----	F	Q	F	Q	G	Q	P	N	V	I	R	K	I	R	C	T	-----													
			140	*	160	*	180	*																																																							
HsSac1	----	Y	R	V	L	Q	H	S	-----	I	V	S	T	K	F	N	S	R	I	D	S	E	E	A	E	Y	I	K	----	L	L	E	L	H	L																												
HmhSac2	LL	K	T	F	T	H	I	K	S	N	-----	V	S	A	P	N	K	K	V	K	E	S	K	E	K	E	K	L	E	R	----	L	L	E	E	L	K	M	F	M																							
SPsyj	---	D	H	I	R	Q	E	N	-----	Y	S	P	D	I	P	D	G	Y	D	T	D	T	Q	G	Y	D	S	Y	K	-----	Y	A	A	E	P	F	S	S	L	R	K	L	L																				
ScINP52p	---	D	F	M	D	I	D	S	S	G	P	I	V	T	N	D	G	D	F	A	I	S	S	P	P	S	I	S	T	H	S	S	R	S	S	S	R	S	L	N	A	Q	E	Q	A	P	K	H	P	C	H	E	L	R	K	L	L						
Dd5P3Sac	---	D	F	I	S	F	Q	T	G	-----	R	G	H	I	S	I	G	G	G	G	G	G	G	S	G	N	G	E	S	K	-----	E	D	D	R	P	Y	V	Q	V	M	N	L	L																			
			200	*	220	*	240	*	260																																																						
HsSac1	KN	S	T	F	Y	F	S	---	Y	T	Y	D	L	T	N	S	L	Q	R	N	---	E	K	V	G	P	A	A	S	W	K	T	A	D	E	R	F	F	W	N	H	Y	L	T	E	D	I	R	N	F	A	H	Q	----	D	P							
HmhSac2	D	S	E	S	F	Y	Y	S	---	L	T	Y	D	L	T	N	S	V	Q	R	S	T	G	E	R	D	G	-R	P	L	W	Q	K	V	D	D	R	F	F	W	N	K	Y	M	I	Q	D	L	T	E	I	G	T	-----	P								
SPsyj	T	N	G	S	F	Y	F	S	---	L	D	F	D	I	T	T	R	L	Q	L	R	T	-S	Q	T	M	T	E	P	-Q	Y	D	S	M	H	T	Q	F	M	W	N	E	F	M	L	R	Q	L	I	K	F	R	S	H	L	N	G	D	E	K	S		
ScINP52p	S	N	G	S	F	Y	Y	S	---	T	D	F	D	L	T	C	T	L	Q	K	R	--	G	F	T	E	H	S	L	-S	F	D	D	F	D	R	E	F	M	W	N	S	F	L	M	D	E	I	I	T	Y	R	D	R	L	D	V	T	A	K	E		
Dd5P3Sac	N	S	G	H	F	Y	W	T	P	P	N	S	S	F	D	I	T	R	Y	Q	S	Q	C	-L	E	P	K	S	D	L	P	V	W	E	R	V	D	K	R	F	Y	W	N	K	Y	L	Q	K	D	F	I	A	Y	R	-----								
		*	280	*	300	*	320	*																																																							
HsSac1	R	I	D	S	F	I	Q	P	--	V	I	Y	G	Y	A	K	I	V	D	A	-V	L	N	-----	A	T	P	-----	I	V	L	G	L	I	T	R	R	S	I	F																							
HmhSac2	D	V	D	F	W	I	I	P	--	M	I	Q	G	F	V	Q	I	E	E	L	-V	V	N	Y	T	E	S	S	D	D	E	K	S	P	E	T	P	P	Q	E	S	T	C	V	D	I	H	P	R	F	L	A	L	I	S	R	R	S	R	H			
SPsyj	A	L	D	G	C	R	F	F	T	C	A	I	R	G	F	A	S	T	E	Q	F	-K	L	G	-----	I	Q	T	-----	I	R	L	S	L	I	S	R	L	S	S	L																						
ScINP52p	L	L	D	Q	R	G	F	L	T	T	V	I	R	G	F	A	E	T	I	F	S	-Y	I	N	-----	R	L	K	-----	V	G	L	T	I	I	S	R	Q	S	W	K																						
Dd5P3Sac	L	Y	D	-	W	C	F	P	--	I	I	Q	G	F	V	S	D	H	L	G	H	I	Q	-----	G	K	N	-----	V	V	Y	T	L	I	S	R	R	S	R	F																							
		*	340	*	360	*	380	*																																																							
HsSac1	R	A	G	T	R	F	R	G	V	D	K	D	G	N	V	G	N	F	N	E	T	E	Q	I	L	L	A	E	N	P	E	S	E	K	I	H	V	F	S	F	L	Q	T	R	G	S	V	P	I	Y	W	A	E	I	N	N	L	K	Y	K	P	N	L
HmhSac2	R	A	G	M	R	Y	K	R	R	G	V	D	K	N	G	N	V	A	N	Y	V	E	T	E	Q	L	I	H	V	H	N	-----	H	T	L	S	F	V	Q	T	R	G	S	V	P	V	F	W	S	Q	V	G	-Y	R	Y	N	P	R	P				
SPsyj	R	A	G	T	R	F	L	S	R	G	V	D	D	G	N	V	A	N	F	V	E	T	E	T	I	L	D	S	S	K	Y	-----	C	V	S	Y	C	Q	V	R	G	S	I	P	I	F	W	E	Q	E	G	V	Q	M	F	G	Q	K	I				
ScINP52p	R	A	G	T	R	F	N	A	R	G	I	D	D	D	G	H	V	A	N	F	V	E	T	E	M	I	M	Y	S	S	Q	Y	-----	C	Y	A	F	T	Q	I	R	G	S	L	P	I	F	W	E	Q	D	-T	S	L	I	S	P	K	I				
Dd5P3Sac	R	A	G	T	R	F	V	T	R	G	I	D	D	D	G	N	V	A	N	F	C	E	S	E	Q	I	L	S	I	E	S	Y	G	----	V	L	A	F	L	Q	I	R	G	S	V	P	V	F	W	N	Q	S	S	P	Q	M	S	D	L	K	I		
			400	*	420	*	440	*																																																							
HsSac1	V	L	G	-----	E	N	S	L	D	A	T	K	-K	H	F	D	Q	Q	K	E	L	Y	G	D	N	Y	L	V	N	L	V	N	-Q	K	G	H	E	L	P	V	K	E	G	Y	E	S																	
HmhSac2	R	L	D	-----	R	S	E	K	E	T	V	A	Y	F	C	A	H	F	E	E	Q	L	N	I	Y	K	K	Q	V	I	I	N	L	V	D	-Q	A	G	R	E	K	I	I	G	D	A	Y	L	K														
SPsyj	D	I	T	-----	R	S	L	E	A	T	R	A	A	F	E	K	H	F	T	S	L	I	E	E	Y	G	P	V	H	I	I	N	L	L	G	-T	G	S	G	E	R	S	L	S	E	R	L	R	Q														
ScINP52p	Q	I	T	-----	R	S	V	E	A	T	Q	P	T	F	D	E	H	F	I	R	L	F	K	K	Y	G	P	V	H	I	I	N	L	L	S	-T	K	S	S	E	I	Q	L	S	R	R	Y	K	E														
Dd5P3Sac	K	M	S	N	L	S	K	I	G	K	I	S	K	K	K	I	T	I	A	R	N	T	Q	A	T	T	P	A	F	Q	L	H	L	K	E	Q	T	K	K	Y	G	N	I	V	I	N	L	L	S	K	L	S	G	E	C	D	L	V	N	A	Y	E	E
			460	*	480	*	500	*	520																																																						
HsSac1	V	V	H	A	L	N	D	P	K	I	----	H	Y	V	Y	F	D	F	H	E	C	R	K	M	Q	W	H	R	V	K	L	L	I	D	H	L	E	K	L	G	L	S	N	E	-----	D	F	F	H	K	V	I											

HmhSac2	QVLLFNNSHL-----TYVSFDFHEHCRGMKFENVQTLTDAIYDIIL-----DMKWCWV
SPsyj	HIQLSPEKDL---IHLTEFDYHSQIR--SFEDANKIRPMIYSDAETFG-----FY-FE
ScINP52p	QLKNSEKMKIGRDVFLTSFDFHRETSQDGFAAASRIIPKIRNTILDAG-----YFSYD
Dd5P3Sac	QIRILRSPQV---FYNHFDLNEQTKGNRMDPLDSLINYIDNQSIISGGGGTTGGVSEKIVGYFFQ

		*	540	*	560	*	580
HsSac1	DSNGNTVEIVNEQHSVVRINCMDCLDRTNVVQSVLAQWVLOKEFESADVATGSTWEDNAPLLTS						
HmhSac2	DEAG----VICKQEGIFRVNCDCLDRTNVVQAATARVVMEQQLKKLGVMPEQPLP--VKCNRI						
SPsyj	NNEG---QSIVVQDGVFRTNCLDCLDRTNVIQNLVSRVFLEQVMIYTRQNAGYDFW-----QV						
ScINP52p	VKEG---RLISEQDGVFRTNCLDCLDRTNLIQQTISLAVFKLFLEDFRLVKPSSFIDDN-EFVQK						
Dd5P3Sac	NSNG---QIISKQNGIIRTNCKDCLDRTNIVQSRVSWVLFESQLRKLGIFRGHDSIGSYPRVSQT						

	*	600	*	620	*	640	*
HsSac1	YQNLWADNADAVSVAYSGTGALKTDFTRTGKRTRLGAFNDFLNSASRYYQNNWTDGPRQDSYDLF						
HmhSac2	YQIMWANNGDSISRQYAGTAALKGDFTRTGERKLAGVMKDGVNSANRYYLNRFKDAYRQAVIDL						
SPsyj	HSTIWANNGDALARIYTGAGALKSSFTRKGKLSIAGALNDLSKSVGRMYINNFQDKGRQETIDLL						
ScINP52p	VNALWADNGDQISQIYTGATNALKSSYSRKKGMSFSGALSDATKSVSRMYINNFVDKKGQQNIDTL						
Dd5P3Sac	LKTTWADNGDALSIQYAGSGSLKSTLTREGDYGIMGMLADGKKTMTRFYINNFEDPGRQDVLDLL						

HsSac1	LG
HmhSac2	QG
SPsyj	LG
ScINP52p	LG
Dd5P3Sac	LG

Appendix E: Primers mentioned in Materials and Methods

1OES2	AATTAGGATCCAAAAATGTTAATAGTTTTTTAGAAGGAG
1OER1	TTTATAAGATCTTTACTCCTCATTGTCAACCATATC
2OES1	TTATAGGATCCAAAAATGAATGGATTAATGGGTAG
2OER1	TTATAAGATCTTTAAACTGGAGAGAAATGATGAG
4OES1	AATTAGGATCCAAAAATGGGTGATATTCAAATACAG
4OER1	ATATAAGATCTTTAATCTGGCATACTACTATTCTC
5OES2	TTATACTCGAGAAAAATGAATGGTAGTGGTCATGATG
5OER2	ATATTCTGCAGTTAAAGATTATTGGTACTTTGAGAGG
5P2S1	TGATGAATTCAGTAAAAGCAACAGCAGCC
5P2R1	ACAATCTAGAGCTTTCGTTTCAGAGTAAGG
5P5S1	ATTGCTGCAGAATCATCACAATTGGTAGG
5P5R1	TGTTACTAGTAACCATTTGAACACTCTACG
5P4S1	CATCTCTAGAGCTGGAGCAGTATTTGAAGG
5P4R1	CACAACTAGTTTGTTTCATCTAGCTTTGG
6BIr	TTACTCTTTATATGCATTAGCACC
6BIr	ATACATCGATGAGAAGCAACG
OE4GAPs1	AATTAGGATCCAAAAATGTCAACAAATGAATCAATGGATG